

OIPF

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,739

DATE: 05/03/2001
TIME: 11:57:22

Input Set : N:\Crf3\RULE60\09828739.txt
Output Set: N:\CRF3\05032001\I828739.raw

3 <110> APPLICANT: Ashkenazi, Avi J.
4 Chuntharapai, Anan
5 Kim, K. Jin
7 <120> TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
8 CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
10 <130> FILE REFERENCE: P1468R1 (REVISED)
12 <140> CURRENT APPLICATION NUMBER: 09/828,739
13 <141> CURRENT FILING DATE: 2001-04-09
15 <150> PRIOR APPLICATION NUMBER: US 09/329,633
16 <151> PRIOR FILING DATE: 1999-06-10
18 <150> PRIOR APPLICATION NUMBER: US 60/089,253
19 <151> PRIOR FILING DATE: 1998-06-12
21 <160> NUMBER OF SEQ ID NOS: 2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1799
25 <212> TYPE: DNA
26 <213> ORGANISM: human
28 <400> SEQUENCE: 1
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31 gcgcccacaa aatacaccga cgatgcccgga tctactttaa gggctgaaac 100
33 ccacgggcct gagagactat aagagcggtc cctaccgcca tggaaacaacg 150
35 gggacagaac gccccggcgg cttcgggggc ccggaagagg cacggccccag 200
37 gacccaggga ggcgcgggga gccaggcctg ggctccgggt cccaagacc 250
39 cttgtgctcg ttgtcgccgc ggctcctgctg ttggtctcag ctgagtctgc 300
41 tctgatcacc caacaagacc tagctcccca gcagagagcg gccccacaac 350
43 aaaagaggtc cagccctca gagggattgt gtccacctgg acaccatatac 400
45 tcagaagacg gtagagattg catctcctgc aaatatggac aggactatag 450
47 cactcactgg aatgacctcc ttttctgctt gcgctgcacc aggtgtgatt 500
49 caggtgaagt ggagctaagt ccctgcacca cgaccagaaa cacagtgtgt 550
51 cagtgcgaag aaggcacctt ccgggaagaa gattctcctg agatgtgccg 600
53 gaagtgcgcg acagggtgtc ccagagggat ggtcaaggtc ggtgattgta 650
55 caccctggag tgacatcgaa tgtgtccaca aagaatcagg catcatcata 700
57 ggagtcacag ttgcagccgt agtcttgatt gtggctgtgt ttgtttgcaa 750
59 gtctttactg tggagaaaag tccttcctta cctgaaaggc atctgctcag 800
61 gtggtggtgg ggacctgag cgtgtggaca gaagctcaca acgacctggg 850
63 gctgaggaca atgtcctcaa tgagatcgtg agtatcttgc agcccaccca 900
65 ggtccctgag caggaaatgg aagtccagga gccagcagag ccaacagggtg 950
67 tcaacatggt gtcccccggg gagtccagagc atctgctgga accggcagaa 1000
69 gctgaaaggc ctcagaggag gaggctgctg gttccagcaa atgaagggtga 1050
71 tcccaactgag actctgagac agtgcttcga tgactttgca gacttggtgc 1100
73 cctttgactc ctgggagccg ctcatgagga agttgggcct catggacaat 1150
75 gagataaagg tggctaaagc tgaggcagcg ggccacaggg acaccttgta 1200
77 cagcatgctg ataaagtggg tcaacaaaac cgggcgagat gcctctgtcc 1250
79 acaccctgct ggatgccttg gagacgctgg gagagagact tgccaagcag 1300
81 aagattgagg accacttggt gagctctgga aagtccatgt atctagaagg 1350
83 taatgcagac tctgccwtgt cctaagtgtg attctcttca ggaagtgaga 1400
85 ccttcctggt ttacctttt ttctggaaaa agcccaactg gactccagtc 1450

ENTERED

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87 agtaggaaag tgccacaatt gtcacatgac cgtactgga agaaactctc 1500
89 ccatccaaca tcacccagtg gatggaacat cctgtaactt ttactgcac 1550
91 ttggcattat ttttataagc tgaatgtgat aataaggaca ctatggaaat 1600
93 gtctggatca ttccgtttgt gcgtactttg agatttggtt tgggatgtca 1650
95 ttgttttcac agcacttttt tatcctaata taaatgcttt atttatttat 1700
97 ttgggctaca ttgtaagatc catctacaaa aaaaaaaaaa aaaaaaaaaa 1750
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101 <210> SEQ ID NO: 2

102 <211> LENGTH: 411

103 <212> TYPE: PRT

104 <213> ORGANISM: human

106 <220> FEATURE:

W--> 107 <221> NAME/KEY: xaa

108 <222> LOCATION: 410

109 <223> OTHER INFORMATION: xaa = leu or met

111 <400> SEQUENCE: 2

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112 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
113   1           5           10           15
115 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
116           20           25           30
118 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
119           35           40           45
121 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
122           50           55           60
124 Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
125           65           70           75
127 Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
128           80           85           90
130 Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
131           95          100          105
133 His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
134          110          115          120
136 Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
137          125          130          135
139 Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140          140          145          150
142 Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
143          155          160          165
145 Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
146          170          175          180
148 Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
149          185          190          195
151 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
152          200          205          210
154 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
155          215          220          225
157 Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
158          230          235          240
160 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val

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161		245		250		255
163	Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly					
164		260		265		270
166	Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro					
167		275		280		285
169	Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala					
170		290		295		300
172	Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp					
173		305		310		315
175	Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg					
176		320		325		330
178	Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu					
179		335		340		345
181	Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp					
182		350		355		360
184	Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp					
185		365		370		375
187	Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu					
188		380		385		390
190	Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn					
191		395		400		405
W--> 193	Ala Asp Ser Ala Xaa Ser					
194		410				

VERIFICATION SUMMARY

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L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2